Original article

Genetic parameters for lactation traits of milking ewes: protein content and composition, fat, somatic cells and individual laboratory cheese yield

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Abstract – The effects of some environmental variation factors and the genetic parameters for total milk traits (fat content, protein content, casein content, serum protein content, lactation mean of individual laboratory cheese yield (**LILCY**), lactation mean of somatic cell count (**LSCC**), and milk yield) were estimated from the records of 1 111 Churra ewes. Genetic parameters were estimated by multivariate REML. Heritability for fat content was low (0.10) as is usually found in the Churra breed. Heritabilities for protein content, casein content, serum protein content, LILCY, milk yield and somatic cell count were 0.31, 0.30, 0.22, 0.09, 0.26 and 0.11, respectively. The highest heritability estimates were for protein and casein contents. Casein content is not advisable as an alternative to protein content as a selection criterion for cheese yield improvement; it does not have any compelling advantages and its measurement is costly. Our results for LSCC indicated that efforts should focus on improving the level of management rather than selecting for somatic cells, in the actual conditions of the Churra breed.

dairy ewes / casein content / individual laboratory cheese yield / genetic parameters / selection goal

Abbreviation key: LILCY = lactation mean of individual laboratory cheese yield; **LSCC =** lactation mean somatic cell count (in their natural logarithmic form); **FYS =** flock-year-season; **L30-120 =** milk yield obtained between 30 and 120 days.

1. INTRODUCTION

Interest in research into the yield and composition of milk from small ruminants in general has increased in recent decades because of the growing

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intensification of sheep and goat production systems [24, 29] and the initiation of breeding programmes [22]. The protein content and composition of sheep milk are important to the cheese manufacturer and are considered a major factor in determining the yield and quality of the final product.

Selecting for casein content would constitute a change in breeding goals from the current practice of selecting firstly for milk yield and secondly for fat content and/or protein content. Although there are numerous estimates for milk yield and fat traits, corresponding information on protein traits is restricted to crude or true protein. No heritability estimates were found for casein and serum protein contents nor their genetic relationships with other milk traits. The estimation of genetic parameters for casein content would help in re-examining the selection programmes in the future.

The individual laboratory cheese yield (**ILCY**) is one variable that can be determined for each milk sample of milk recording [38]. Thus, it is of great interest to estimate the genetic parameters of the lactation mean of individual laboratory cheese yield for this trait (**LILCY**) and its genetic and phenotypic relationships with milk traits. This estimator could improve selection decisions for sheep breeds, since cheese yield relies mainly on the milk components.

The somatic cell count is a good indicator of the existence of subclinical mastitis [25], and some studies on dairy cows associated the variation of protein content and composition to a change in somatic cell count [3, 5, 49]. Nevertheless, little information is available on the genetic parameters of lactation measures for somatic cell count (**LSCC**) or the relationships between LSCC and yield or the composition of the milk of dairy ewes [7, 17].

The objective of our study was to estimate the genetic parameters for lactation measures of fat, protein, casein and serum protein contents, LILCY and LSCC. Environmental factors, heritabilities, repeatabilities, and genetic and phenotypic correlations among these variables were estimated using a multitrait repeatability animal model.

2. MATERIALS AND METHODS

2.1. Data

Data were collected on dairy farms from three regions in Castile and León, Spain. A total of 1 962 lactation records were obtained, between April 1997 and July 1999, from 1 111 Churra ewes belonging to eight flocks at the Churra selection nucleus. All flocks were on the alternate a.m.-p.m. plan of testing and all ewes were milked twice daily.

According to the testing programme applied for Spanish dairy ewes, milk yield is defined by the production during the milking period only, beginning after one month of suckling. Accordingly, only the decreasing part of the lactation curve is recorded while the milk solid contents are increasing throughout

that period. The first test day record was obtained at least 3 d after weaning (between the 31st and 75th d postpartum). Subsequent records were obtained at approximately monthly intervals thereafter.

Previous studies on indigenous Spanish breeds have shown very low heritability estimates for fat content [8, 34]. Data originating in the milk recording schemes always give much lower heritability and repeatability estimates than those reported for other components such as protein content [14, 34]. The three factors most likely to cause such results are management conditions (dependent on the stockbreeder's knowledge), data collection or a possible inadequate analysis of milk samples. In this study, we collected, transported and analyzed milk samples in the dairy plant of León University in order to avoid the effects of collection, transport and analysis of samples on the genetic estimates for fat content in Churra ewes. Analyses for fat and protein contents and composition were determined by a AEGYS MI 200 spectrometer (ANADIS®, Trappes, France) based on the mid infrared FTIR method (Fourrier Tranformed InfraRed) and were calibrated against known sample standards. Test day ILCY (individual laboratory cheese yield), expressed in kg per 100 L of milk, was measured from individual milk samples (10 mL), compatible with milk recording in dairy sheep. ILCY was measured as described by Othmane [38]: preheated and homogenised milks were curdled at 37 °C for 1 h. In order to facilitate rennet distribution in the milk, the rennet was diluted 10-fold with bidistilled water before addition to the milks. ILCY was thus measured, the coagulum (cottage cheese + whey) being centrifuged for a standard time of 15 min at 2 500 rpm after longitudinal cutting and the whey being removed after draining for 45 min with the test-tube face downward (the curd remained quiescent at the bottom of the tube). ILCY was defined as the weight of the centrifuge residue (curd obtained after expulsion of whey and draining in the open air) expressed in kg per 100 L of milk.

Milk yield per lactation, estimated and adjusted to 90 d (**L30-120**) using the Fleischmann method, was provided by the National Association of Spanish Churra Breeders (ANCHE) as well as the test day records for somatic cell count. The SCC were determined using the Fossomatic method as described by Gonzalo *et al.* [23]. Test day records of somatic cell count were transformed to their logarithmic form [2]. From the ANCHE data file other available pertinent information included the date of milk sampling, number of suckled lambs, date of birth of the ewe and lambing date.

Lactation measures of milk composition traits (fat content, protein content, casein content, serum protein content, LSCC and LILCY) were obtained as the means of the corresponding monthly test day records preadjusted for stage of lactation and morning-evening test date using additive factors [17]. These correction factors were obtained by employing a fixed model that included the fixed effects: test date record (a.m. or p.m.), flock test date nested to test

day record (130 levels), stage of lactation (6 levels), age of ewe (4 levels) and
lambing type (one lamb or more).

The mean number of test day records per lactation was 3.76 (696, 1 045, 216
and 5 lactations with 3, 4, 5 and 6 records, respectively) and mean lactation
records per ewe were 1.77. The animals included in the relationship matrix
(two generations) were 2 021 ewes and 184 rams. The rams included 59 non-AI
rams, 85 AI rams with $\geq$ 10 daughters in the data file and 40 rams with less
than 10 daughters. Some ewes (123) having their own data were also listed as
the dams of ewes. All pedigree data were verified using DNA genetic markers
as described by Bragança *et al.* [10].

2.2. Statistical analysis

Data were gathered according to the different levels of the main environ-
mental variables that were thought to affect milk yield and composition in the
Churra breed conditions [11]. There were four lambing age groups (1: between
1 and 2 yrs; 2: between 2 and 3 yrs; 3: between 3 and 4 yrs; and 4: over 4 yrs),
two types of lambing (single or multiple), and 41 levels of flock-year-season
(**FYS**) of lambing. Each year was divided into three seasons: January to March,
April to June, and July to December.

All known relationships among individuals were considered in the model of
analysis that included the previous fixed effects. The dependent variables were
fat, protein, casein and serum protein contents, LSCC, L30-120 and LILCY.
Data of these lactation measures were analysed with the following multitrait
repeatability animal model:

$$Y_{ijklm} = \mu + FYS_i + LG_j + LT_k + A_l + PE_l + e_{ijklm}$$

where

Y_{ijklm} = dependent variable;
μ = population mean;
FYS_i = fixed effect of flock-year-season i;
LG_j = fixed effect of lambing age j;
LT_k = fixed effect of lambing type k;
A_l = additive genetic random effect of the individual l;
PE_l = permanent environmental random effect on the individual l;
e_{ijklm} = random residual.

Genetic parameters were estimated by the REML (restricted maximum
likelihood estimation) [36] using the VCE package [28]. The environmental
effects were estimated by the GLM and VARCOMP procedures using the
Statistic Analysis System programme, SAS® package [43]. The fixed effects
were treated as random in the VARCOMP procedure. The proportion of

Table I. Arithmetic means ($\bar{x}$), standard deviations (SD) and residual standard deviations (RSD) of the lactation traits.

Trait	$\bar{x}$	SD[1]	RSD[2]
Milk yield (L30-120) (L)	93	30.9	23.9
Fat content (g $\cdot$ L^{-1})	74.9	10.5	9.3
Protein content (g $\cdot$ L^{-1})	61.1	4.7	3.6
Casein content (g $\cdot$ L^{-1})	48.4	4.1	3.2
Serum protein content (g $\cdot$ L^{-1})	12.1	0.8	0.7
LILCY[3] (kg $\cdot$ 100 L^{-1})	27.2	3.2	2.9
LSCC[4]	12.1	1.3	1.0

[1] Derived from the sum of the additive genetic, permanent environmental, and residual variances obtained from the VCE analysis.
[2] From VCE.
[3] LILCY = lactation mean of individual laboratory cheese yield.
[4] LSCC = lactation mean of somatic cells (in their natural logarithmic form).

variance explained by the FYS factor was calculated by dividing the variance component of the FYS factor by the sum of the residual and FYS variance.

3. RESULTS

The means for milk yield, fat content, protein content, casein content and serum protein content (Tab. I) were within the range of estimates that have been recorded for dairy sheep in the Mediterranean countries [20, 33, 40]. The LSCC obtained from the current study coincided with the previous results reported for Churra ewes and were higher than those reported for Lacaune ewes [7] and for dairy cows [13, 18]. No studies have been carried out on the individual cheese yield on a laboratory scale from the milk amounts compatible with those usually collected according to the milk recording scheme (50 mL). The LILCY value obtained from this study coincided with those reported for real cheese yield in dairy ewes [4, 41]. However, the yield of laboratory-scale cheese, like cottage cheese, tended to be higher than that of ripened cheese [32] as expected. This was probably attributable to the very reduced milk amounts employed and the forced draining (centrifugation) of the cottage cheese, which captures even the smallest curd that may be lost with the whey in the industrial process.

3.1. Environmental variation factors

Flock-year-season (FYS) and age of the ewe at lambing contributed significantly ($P < 0.001$) to the variations in milk yield, fat, protein, casein,

Table II. Least square means of total milk traits by age of ewe and lambing type.

Variable	Ewe's age				Lambing type	
	1–2 yr	2–3 yr	3–4 yr	> 4 yr	1	> 1
Milk yield (L30-120) (L)	93[c]	93[c]	101[b]	106[a]	94[b]	102[a]
Fat content (g · L^{-1})	67.4[c]	67.8[c]	70.2[b]	72.4[a]	70.4[a]	68.5[b]
Protein content (g · L^{-1})	58.1[b]	59.6[a]	60.5[a]	60.3[a]	59.6	59.6
Casein content (g · L^{-1})	46.0[b]	47.2[a]	48.0[a]	47.8[a]	47.2	47.2
Serum Protein content (g · L^{-1})	11.6[b]	12.0[a]	12.1[a]	12.0[a]	11.9	12.0
LILCY[1] (kg · 100 L^{-1})	26.7[b]	26.6[b]	27.1[a]	27.3[a]	27.0	26.9
LSCC[2]	11.9	12.3	12.1	12.2	12.1	12.2

[a,b,c] Means in a row (within variation factor) with different superscripts differ ($P < 0.05$).
[1] LILCY = lactation mean of individual laboratory cheese yield.
[2] LSCC = lactation mean of somatic cells (in their natural logarithmic form).

serum protein and LILCY. The LSCC was significantly affected ($P < 0.001$) by FYS but was not affected by lambing age. The lambing type effect was significant ($P < 0.01$) for milk yield and fat content and not significant for protein fractions, LILCY and LSCC.

The FYS factor became the major variation factor for all variables. It accounted for 27%, 26%, 27%, 28%, 38%, 19% and 100f the phenotypic variance in fat content, protein content, casein content, serum protein content, LILCY, milk yield and LSCC, respectively. Similar results for milk yield, protein content and LSCC were reported for the same breed [17]. No results had been reported for the rest of the variables. These results demonstrated the importance of the FYS environmental effect for genetic models with lactation variables.

Table II shows the effect of lambing age and lambing type on the variables studied. All variables except LSCC were affected by the age of the ewe at lambing. The youngest ewes produced the least amount of milk which was also the least rich in fat, protein, casein and serum protein contents. As the ewes became older, there was an increase in fat and protein contents and the milk yield was higher. Accordingly, the highest LILCY were obtained from the oldest ewes, and vice versa. LSCC was not altered by the age of the ewe. Although such a result may be unexpected, Sevi *et al.* [45] have also recently reported that somatic cell counts in Comisana ewes' milk and the prevalence of subclinical mastitis were not changed by parity. In our study, this fact can be explained by the major mastitis control routinely applied to the flocks used: teat dip after milking, selective dry therapy, and culling of ewes with chronic mastitis.

Table III. Heritabilities (h^2), proportions of permanent environmental variance (c^2), their standard error (SE), and repeatabilities (r) for total milk traits.

Trait	h^2	SE	c^2	SE	r
Milk yield (L30-120) (L)	0.26	0.03	0.14	0.03	0.40
Fat content ($g \cdot L^{-1}$)	0.10	0.03	0.11	0.03	0.21
Protein content ($g \cdot L^{-1}$)	0.31	0.03	0.07	0.03	0.38
Casein content ($g \cdot L^{-1}$)	0.30	0.03	0.07	0.03	0.37
Serum protein content ($g \cdot L^{-1}$)	0.22	0.02	0.04	0.02	0.26
LILCY[1] ($kg \cdot 100\ L^{-1}$)	0.09	0.02	0.07	0.02	0.16
LSCC[2]	0.11	0.03	0.23	0.04	0.34

[1] LILCY = lactation mean of individual laboratory cheese yield.
[2] LSCC = lactation mean of somatic cells (in their natural logarithmic form).

Lambing type had a significant effect on milk yield and fat content and a non-significant effect on protein fractions, LSCC and LILCY. This result agrees with others on Churra [12, 17, 20] and Latxa [21] ewes for fat and protein contents and somatic cells. Ewes that gave birth to multiple lambs had a higher milk yield (102 L) than ewes that gave birth to singletons (94 L). The physiological explanation of this fact is that a high number of lambs corresponds to a greater placenta area which results in higher mammary hormone level and a more developed udder [16].

3.2. Heritability and repeatability coefficients

Table III presents the heritabilities, permanent environmental variance proportions, and repeatabilities for lactation traits studied. Heritability and repeatability estimated for milk yield from this study (0.26 and 0.38) coincided with the other results previously reported for the same breed [12, 17] and other dairy ewes [42, 44]. Estimates for fat content remained low in spite of precautions taken in sampling and milk analysis at our dairy plant. Heritability and repeatability of fat content were especially low (0.10 and 0.21, respectively), as were those obtained by Jurado *et al.* [34] in the Spanish Manchega breed. We think that our results were probably influenced by the enormous variability in conditions of milking practice and management in general for the Churra breed (hand stripping, nutrition, *etc.*), the possible effects of sample collection and analysis being discarded. Heritability estimated for protein content (0.31) was higher than our previous result (0.17) in the same breed [17] and lower than the results reported for other breeds [7, 15, 42]. Greater values were reported for the Lacaune breed, with the methods of management being more uniform, the production level higher and only the first lactation records being normally

used. The heritability of adjusted LSCC obtained from this study was 0.11. This value was below the heritability estimates reported for dairy cattle [13,35, 50], which is likely to be due to the smaller number of test-days per lactation in dairy ewes. However, we know of only two previous studies on the genetic parameters for lactation mean of SCC in dairy ewes. These estimates were obtained from flocks in the Churra and Lacaune breeds. The first one, involving both heritability and repeatability [17], gave estimates similar to ours. The second study, including only heritability in first lactation [7], reported higher estimates (0.15 to 0.18).

There were no previous genetic studies for protein fractions or individual cheese yield in dairy ewes. The casein content in milk was assumed to be a major factor determining cheese yield and quality [31,37] but there was no available information on its inheritance and genetic relationships, with protein content and cheese yield allowing it to be judged as a selection criterion. In our study, the highest heritabilities corresponded to protein content and composition (Tab. III). Heritabilities and repeatabilities for protein and casein contents were similar and relatively high. Furthermore, both traits had a comparable genetic variation coefficient (4.3% and 4.6%, respectively). A lower heritability (0.22) and repeatability (0.26) were found for serum protein content, since the changes in protein composition by the various environmental factors are more manifest in the case of serum protein content than in that of casein or protein content [26,30].

Estimates of heritability and repeatability for LILCY obtained under Churra breed conditions seemed particularly low (0.09 and 0.16, respectively) in comparison with the other milk components. Such results were probably influenced by those of fat content. The cheesemaking ability undoubtedly depends on the main milk components, though it could also possibly be considered as a function of several other factors difficult to identify at times, such as rennet strength, atmospheric conditions, etc. Our interpretation may explain in part the high phenotypic and environmental variability (not shown) observed for this trait as well as for fat content.

3.3. Genetic and phenotypic correlations

Genetic and phenotypic correlations among lactation traits are given in Table IV. Correlations between milk yield and qualitative traits were clearly negative, suggesting that selection by milk yield is expected to be associated with a reduction in fat content, protein content, casein content and LILCY. Thus, these negative associations might imply the necessity of including content traits in selection programmes if their levels are to be maintained while increasing milk yield. For milk composition, both genetic and phenotypic correlations were high and positive, usually with the genetic correlation being higher than the phenotypic correlation. This pattern is often found [6,7,17]

Table IV. Genetic [†] (lower triangle) and phenotypic (upper triangle) correlations among total milk traits.

Trait	L30-120	TF	TP	TC	SP	LILCY	LSCC
Milk yield (L30-120) (L)		−0.09	−0.04	−0.01	−0.12	−0.11	−0.16
Total fat content (TF) (g · L^{-1})	−0.56		0.48	0.50	0.22	0.41	0.03
Total protein content (TP) (g · L^{-1})	−0.64	0.85		0.99	0.66	0.29	0.14
Total casein content (TC) (g · L^{-1})	−0.65	0.85	0.99		0.55	0.29	0.12
Serum Protein content (SP) (g · L^{-1})	−0.59	0.81	0.96	0.96		0.09	0.14
LILCY [1] (kg · 100 L^{-1})	−0.59	0.80	0.85	0.86	0.73		0.05
LSCC [2]	−0.17	−0.08	0.15	0.12	0.31	0.30	

[1] LILCY = lactation mean of individual laboratory cheese yield.
[2] LSCC = lactation mean of somatic cells (in their natural logarithmic form).
[†] Standard errors of genetic correlations ranged from 0.06 to 0.13.

with the usual traits (milk, fat and protein). Our estimates of the phenotypic correlations were in the range of 0.22 to 0.99, whereas the genetic counterparts were in the range of 0.81 to 0.99. Estimates of the phenotypic correlations confirmed the results of some previous studies [20, 39]. However, our estimates were slightly more positive between casein and serum protein contents. For the genetic correlations, there were no previous results on this topic for comparison. A high correlation coefficient was close to unity (0.99) found between casein and protein contents. We must bear in mind that protein and casein contents had the highest and very close heritabilities and presented similar correlations with the rest of the variables (Tab. IV). The correlated responses in the main milk components and in LILCY are expected to be similar when selection is by casein or protein content, with the latter being readily available from standard milk recording. In principle, such results detract interest from casein content as a selection criterion for higher cheese yield.

Fat content had high, positive correlations with protein content and composition and LILCY, the highest being with protein and casein contents. The high level of association between fat and protein contents (0.85) is of great interest for the Spanish breed selection programmes where genetic estimates for fat content have been much lower than those reported for other dairy sheep breeds as mentioned above.

The genetic correlation between milk yield (L30-120) and somatic cells (LSCC) was negative (-0.17) and consistent with that reported for the same breed [17]. However, Barillet *et al.* [7] reported a low, positive association (0.07 and 0.09 for the sire model and animal model, respectively) for Lacaune ewes. These correlations depend, in part, on the degree of infection within the population that we are dealing with. In fact, in spite of the strict mastitis control measures and the general high level of husbandry applied to the flocks used in this study, the arithmetic average SCC ($749\,000$ cell $\cdot$ mL^{-1}) duplicated that reported by the same authors in the Lacaune breed ($375\,000$ cell $\cdot$ mL^{-1}), with only 10% infected ewes in first lactation.

It is commonly assumed that milk from a teat affected by mastitis is richer in nitrogenous matter [3, 20, 27, 41, 49]. An increase in the protein fractions was in fact accompanied by an increase in LSCC. A higher correlation was observed with serum protein content (0.31) than with whole protein (0.15) or casein content (0.12), as is usually found in the literature. This association is generally explained by a greater permeability of the udder epithelial membrane to blood protein in the case of infection. The positive correlation between LSCC and casein content was probably due to a temporal increase in the casein ratio in the case of acute mastitis because of the massive destruction of acinar cells which liberate casein in larger quantities [27]. Such a result could also be explained by the decrease in milk production in the case of mastitis.

As expected, LILCY showed negative correlations with milk yield and positive and high correlations with protein fractions and fat. However, its relationships with LSCC did not show a specific pattern from a phenotypic and genetic point of view. The phenotypic estimate was positive but very close to zero (0.05), suggesting that LILCY and LSCC were essentially independent. However, the genetic correlation between both traits was positive and relatively high, a result that would follow from the positive correlation between LSCC and protein content and composition.

4. DISCUSSION

On the whole, our estimates fall within the range of the results already published on Spanish dairy ewes for the usual total milk traits, with the estimates for fat content being very low. Our results, however, tend to be lower than others for certain foreign breeds raised under different management conditions. There are, of course, many possible reasons for this trend. Among them is the enormous diversity in management practices that characterise the entire population, low production level, and the relatively recent (barely 15 years) selection programme and their associated consequences. Implementation of an efficient breeding programme over a long period of time, better fulfilment of nutritional needs and diet formulation, and careful attention to mastitis control and milking management for sheep breeds, such as the Sarde and Lacaune, should not be forgotten, although in the latter case only first lactation records were usually used. In this way, available information on dairy cows indicates that heritability estimates increase with a higher production level [48] and decrease with more lactations [9].

As for fat content, we consider that our results were probably influenced by the enormous variability in conditions of milking practice and management in general (hand stripping, nutrition, *etc.*) for the Churra as well as the other indigenous Spanish breeds. It seems that fat content in milk is especially influenced by the type of feed [1, 19, 45–47]. Therefore, heritability and repeatability estimates for fat content were much lower than those reported by Barillet and Boichard [6] and Barillet *et al.* [7] for the French Lacaune breed, where modern husbandry methods using new feeding practices were implemented [40] and the practice of hand stripping died out.

In previous studies, we observed that the ILCY is a useful predictor of real cheese yield, which can be automated by spectroscopy FTIR and then regularly recorded for each ewe-milk recording. In principle, there can be no doubt that this trait is a closer estimate to industrial cheese yield than milk composition measurements. It may therefore be considered as a selection criterion. The LILCY mean obtained in the present study coincided with the results obtained for real cheese yield in dairy ewes. From a genetic point of view, however, selection by LILCY is not advisable because of its low

heritability, low repeatability and high variability in the present conditions of the Churra breed, since these results are undoubtedly influenced by the fat content behaviour. Furthermore, in spite of its clear advantages, the LILCY estimation method also has its limitations and it is important to put it within its context (laboratory conditions, rennet strength, very reduced amount of individual milk, atmospheric conditions, *etc.*). In any case, this study was a first attempt and it is useful to have more information about genetic parameters for this trait and its relationship with the main milk components in the Churra breed and other breeds of dairy ewes.

Once accepted that selection on LILCY is ill-advised, it is reasonable to consider some milk qualitative aspects in order to appreciate traits that might act to improve cheese yield on the individual level and avoid adverse effects on milk composition brought about by selection for milk yield. The magnitude of the negative genetic correlation between milk yield and protein content and between milk yield and casein content suggests that appropriate economic weights for these traits should be determined and the traits should be included in breeding programmes to prevent future genetic deterioration. Our results showed higher heritabilities and repeatabilities for protein and casein contents which also have the highest positive correlation with LILCY. One may ask whether, and how, selection by protein content tends to enrich or to impoverish the casein content in milk and *vice-versa*. On this regard, both traits had a genetic correlation near unity and very close heritability and repeatability values and were equally correlated to LILCY, indicating that protein and casein contents are almost genetically equivalent. Judging by these first results, the whole casein content is not a tempting alternative as a selection criterion. However, similar studies on the casein fractions and their relationships with the individual cheese yield may be of great interest.

From a genetic point of view, it can be pointed out that selection by protein content will also induce an important correlated increase in fat content because of the high association between both traits; it is of course true that such a correlated response may be attenuated by the low genetic standard deviation of fat content (3.3). This result is of great interest for Spanish breed selection programmes in which the genetic parameters for fat content have always been remote from those reported for other dairy ewes.

It is often suggested that health traits could be improved more easily by better management than by selection. Our results support this suggestion. The high level of SCC in the entire population of the Churra breed suggests that most scrupulous control of sanitation of housing and equipment is necessary before any attempt of selection on somatic cells. However, while taking active steps to improve the level of management, farmers may also consider including this trait when selecting service sires for their flocks, as is usually done in dairy cattle (removal of sires when their daughters are predisposed to high SCC).

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